

## **SPECIFICATION AMENDMENT**

Please amend the specification by replacing the paragraphs beginning on page 16, line 17 with the following amended paragraphs:

**FIG. 1A – 1D.** Aligned amino acid sequences of different boPAGs. Each structure was inferred from the sequences of its cDNA. The likely signal sequence is underlined and a known site of propeptide sequence cleavage (ISG ↓RG/DS) for certain PAGs is shown (vertical arrow). Many additional sequences, some from cDNA not containing entire ORF, others differing less than 5% in nucleotide sequence from those shown, are known. Numbering at end of rows is by amino acid residue starting the Met1. Numbers in parentheses show the equivalent residue of pepsin. Boxes indicate the conserved sequences around the catalytic aspartic acid residues (Asp32 and Asp 215). GenBank Accession codes for boPAG1 through boPAG12 are M73961, L06 151, L06 153 and AF020506 through AF 020514, respectively.

Please amend the specification by replacing the paragraphs beginning on page 17, line 1 with the following amended paragraphs:

**FIG. 2A – 2D.** The aligned amino acid sequences of different ovPAGs. See legend to FIG. 1A – 1D for details. GenBank Accession codes for ovPAG1 through ovPAG9 are M73962, U30251 and U94789 through U94795, respectively.